

- C1  
CONT.
3. (Amended) The method of claim 1 wherein the mismatch repair gene is MutS.
4. (Amended) The method of claim 1 wherein the mismatch repair gene is MutL.
5. (Amended) The method of claim 1 wherein the mismatch repair gene is MutY.
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- Sub D4
12. (Amended) The method of claim 3 wherein said polynucleotide encoding a form of a mismatch repair protein comprises a truncation mutation.
13. (Amended) The method of claim 4 wherein said polynucleotide encoding a form of a mismatch repair protein comprises a truncation mutation.
- C2
14. (Amended) The method of claim 6 wherein said polynucleotide encoding a form of a mismatch repair protein comprises a truncation mutation.
15. (Amended) The method of claim 7 wherein said polynucleotide encoding a form of a mismatch repair protein comprises a truncation mutation.
- Sub D4
16. (Amended) The method of claim 4 wherein said polynucleotide encoding a form of a mismatch repair protein comprises a truncation mutation at codon 134.
17. (Amended) The method of claim 6 wherein said polynucleotide encoding a form of a mismatch repair protein comprises a truncation mutation at codon 134.
- Sub D4
18. (Amended) A homogeneous composition of cultured, hypermutable bacteria which comprise a polynucleotide encoding a form of a mismatch repair protein under the control of an inducible transcription regulatory sequence, wherein said polynucleotide exerts a dominant negative effect when expressed in said bacteria.
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- C3 D4
26. (Twice Amended) The homogeneous composition of claim 20 wherein the bacteria express a protein which consists of the first 133 amino acids of PMS2.
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- C4
31. (Amended) The homogeneous composition of claim 23 comprising a protein which consists of a eukaryotic MutS protein.